

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,646
Source: IFWP
Date Processed by STIC: 1/30/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/565,646

CRF Edit Date: 2/2/06
Edited by: in

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other:

inserted amino acid number in sequence 1,3,5



IFWP

RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/565,646

TIME: 18:12:35

Input Set : A:\PTO.AMC.txt

Output Set : N:\CRF4\02022006\J565646.raw

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3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE
5 <120> TITLE OF INVENTION: USE OF THE SILVER GENE FOR THE AUTHENTICATION OF
6     THE ORIGINAL BREED OF ANIMAL POPULATIONS AND
7     THEIR DERIVATIVE PRODUCTS
9 <130> FILE REFERENCE: IFB 03 BT INR SILV
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/565,646
C--> 11 <141> CURRENT FILING DATE: 2006-01-24
11 <160> NUMBER OF SEQ ID NOS: 11
13 <170> SOFTWARE: PatentIn version 3.1
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17 <212> TYPE: DNA
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53 <223> OTHER INFORMATION:
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RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/565,646

TIME: 18:12:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

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78                               1           5
80 ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta ggg acc aca 101
81 Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr
82      10           15           20
84 gaa g gtgagtgtgg gatgttgac atgaacaagt gtgaatttgg ggttgcacac 155
85 Glu
86 25
88 ctgctctggt ttttctctcc ctaaaatgga agatatcagt agtgcttcag gtgtctccca 215
89 cccatttgat ttagtgagga catgggcaac tgagctccct ccccatga agatttgggt 275
90 gcatgtgtgt tcaggcactt gggactgaac ctgaaaacaa ccccatctac ctggatgggt 335
91 gagagaacag tatgtctccg tggccctaata tttgagatgc tctgaatagt gagctggaac 395
92 atgggtgcca aggtagtaaa atgagtggaa actcatttag gctttgtctc aggcacttgg 455
93 gatagggtat ttaggagata gagaaagata ggagatagga gaaaggagaa agaggatgtg 515
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107 ccaaaaaaca aacgaacaac aaaaataaag gatagataaa gcaaatgtga caaaatgctg 1355
108 atagttgttg gaccttgggg agacacatgc agagccatca catcactttt tttcagacat 1415
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112 tcgtctgagg tgccgttgcc tacaggataa agtccaaact cctttgctg gcactccaag 1655

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RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/565,646

TIME: 18:12:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

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115 cagtcgacca gagtgcgaatt tacctgttta aaatctatca ttttgttata cattgtgcat 1835
116 gtctattatg gctcatatta agcaatgcct tggattatag taatttatgt atatgtctat 1895
117 ttcataact ttaacctgaa ccccttcaga accatttctt tttcatttct taagttcttt 1955
118 gcacctagcc cagtgcctgg tacgtcgtgg gtattcagta gattaaaatg cactttaagg 2015
119 aacttccctt gttgtccatc aagtggctaa ggctctgtgc tcccaatgca ggggaccagg 2075
120 gttcaatctc aggtcagga actagatccc acaggtcaca actaagagtt tgcaagccac 2135
121 aactacctga cctcacatgc cacaactaat cgaagatccc tctgtctgca actaagtcct 2195
122 agtgcagtta aatatatttt tttaatgcac tttgaatgtg agaatgaatg atgtgtcaca 2255
123 gacactgttg tcccctgaga agggagtgg taatgatttg agggccctca tagtatatct 2315
125 tccttttttag ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag 2363
126 Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln
127 30 35
129 ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa 2411
130 Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu
131 40 45 50
133 agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc 2456
134 Ser Gln Gly Pro Asp Cys Trp Arg
135 55 60
137 agggaggata tgggtgaaat ggggtggggag gggaacgggg ttgaatgtac ttaggaagat 2516
138 agggaaggaa aaggcataca gggaggagaa gcccaaggagc taattaatgc agctgccctt 2576
140 ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg 2625
141 Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu
142 65 70 75
144 att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc 2673
145 Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser
146 80 85 90
148 caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc 2721
149 Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile
150 95 100 105
152 atc aat g gtgagtacct ctccgctcc tcccgaaggt ccagaatccc tggatatccc 2778
153 Ile Asn
154 110
156 aatgagctca aggaatcctc ctccctctttt tttttttttt tttttacaaa ttatatatgt 2838
157 aacacatatt cactgcagaa aaattagaaa acacagataa accaaaaaga aaaaaaatta 2898
158 tagttcccca aatggggcac agaagacca gtggacatag aagttggata gacttggatt 2958
159 taaactgggt accagtatgt gaccctggac aagtcactga attgttttgt tcttccattc 3018
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164 atcgaacca ggtcctagcc tacagtatta attgatgctg ttatttttac ttttatccca 3318
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DATE: 02/02/2006

PATENT APPLICATION: US/10/565,646

TIME: 18:12:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

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174 ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc caa gaa cct 3847
175 Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro
176 115 120 125
178 gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct 3895
179 Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro
180 130 135 140
184 cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g 3938
185 Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp
186 145 150 155
188 gtaagagttt cccttctctg gcctgtcatt cacacttaaa ttcacttctt cctacctgat 3998
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190 tgactccttc ctcttccaca gcacctagtc aactctatta tacttctttc tgggagccct 4118
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192 atgcaagctt aaactctctg aaataaccat ccttgataca tctcctgacc ttccttctct 4238
193 gggtccatct ctaaccctgc cccagtctcc tttgaccagt aaccccttcc cctactcttc 4298
195 tttccaaaaa cctcag ac caa tac tgg caa gtt ctg ggg ggc cca gtg tct 4349
196 Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser
197 160 165
199 gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg 4397
200 Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met
201 170 175 180
203 gaa gtg act gtc tac cac cgc cgg ggg tcc cag agc tat gtg ccc ctc 4445
204 Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu
205 185 190 195 200
207 gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggaggggac 4496
208 Ala His Ser Ser Ser Ala Phe Thr Ile Thr
209 205 210
211 aaggccagtt gcagggcagg agaaggtggg gaggtctgggc tggacaggaa aggggaaaga 4556
212 ggaaatggtg tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg 4616
213 gcttggagcc cgtgaagggc caggcagctt gggttggttg aaaaatatgg ctgtgaaaga 4676
215 agaagctgac agaaagaaga acttatggtt ctcactttct ctgactccaa tcccag ac 4734
216 Asp
219 cag gtg ccc ttc tct gtg agt gtg tct cag ctg cag gcc ttg gat gga 4782
220 Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly
221 215 220 225
223 agg aac aag cgc ttc ctg aga aag cag cct ctg acc ttt gcc ctc cag 4830
224 Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln
225 230 235 240
227 ctc cat gat ccc agt ggc tat ttg gct ggg gct gac ctt tcc tac acc 4878
228 Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr
229 245 250 255
231 tgg gac ttt ggt gac agt aca ggg acc ctg atc tct cgg gca ctc acg 4926
232 Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr
233 260 265 270 275
235 gtc act cac act tac cta gag tct ggc cca gtc act gca cag gtg gtg 4974
236 Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val
237 280 285 290

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RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/565,646

TIME: 18:12:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

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245 ggc act aca gat agg cat gtg aca act gca gag gct cct gga acc aca      5070
246 Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr
247          310          315          320
249 gct ggc caa gtg cct act aca gaa gtc atg ggc acc aca cct ggc cag      5118
250 Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr Pro Gly Gln
251          325          330          335
253 gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc      5166
254 Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr
255 340          345          350          355
257 aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc      5214
258 Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr Ser Lys Val
259          360          365          370
261 tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg      5262
262 Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr Gly Arg
263          375          380          385
265 aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag      5310
266 Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val Thr Gln
267          390          395          400
269 gga aca act cca gag ctg gtg gag acc aca gct gga gag gtg tcc act      5358
270 Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr
271          405          410          415
273 cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt      5406
274 Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr Glu Gly
275 420          425          430          435
277 act gca g gtaagggggc caccatgaat gagttcatag aggtgggggca tttgtcacag      5463
278 Thr Ala
281 ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag      5523
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283 gaatagatcc agagttcagg aaaccagggt cttctcctag gccaggggta gagagcttat      5643
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286 attctccagg caagaacact ggagtgggtg gccatttcct tctccagggg attttccctg      5823
287 cccagggatt aaaccggaat tggcaggtgg attctttacc cgagccacct agaaagtccc      5883
288 atgtgatcat tagataatac ttatacctca ttttctgatt aagtgtaaac acagaaatct      5943
289 ttctgacacc acttcccacc cctggattcc catcccaaag taggtttacc tgggaattgtg      6003
290 gtaggaatac taaaaagga gaagtgagat agtgacacta tgacttaaca catgtcaaat      6063
291 gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaattc      6123
292 tgactctaac cctgtgactc tggggcagtc atttctcttg ggcctttctt tatcttaaaa      6183
293 aatgagagtt tccagctctt gtctgattct aagcctggat ccagtagctc tgactctacc      6243
294 tggaaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgccctt      6303
296 ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc      6352
297          Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala
298          440          445
300 acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat      6400
301 Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr
302          450          455          460

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/565,646

DATE: 02/02/2006
TIME: 18:12:36

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02022006\J565646.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 823

Seq#:5; Line(s) 1224

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/565,646

DATE: 02/02/2006

TIME: 18:12:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:23
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
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L:1373 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 5

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/565,646

DATE: 01/30/2006

TIME: 16:00:01

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\01302006\J565646.raw

3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE
 5 <120> TITLE OF INVENTION: USE OF THE SILVER GENE FOR THE AUTHENTICATION OF
 6 THE ORIGINAL BREED OF ANIMAL POPULATIONS AND
 7 THEIR DERIVATIVE PRODUCTS
 9 <130> FILE REFERENCE: IFB 03 BT INR SILV
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/565,646
 C--> 11 <141> CURRENT FILING DATE: 2006-01-24
 11 <160> NUMBER OF SEQ ID NOS: 11
 13 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

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 1589 <212> TYPE: DNA
 1590 <213> ORGANISM: Artificial sequence
 1592 <220> FEATURE:
 1593 <223> OTHER INFORMATION: Primer
 1595 <400> SEQUENCE: 11
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 E--> 1605 ¹ delete

**Does Not Comply
 Corrected Diskette Needed**

see pp 1-5

30

from sequence 1

10/565,646 2

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atgtgatcat tagataatac ttatacctca ttttctgatt aagtgtaaac acagaaatct	5943
ttctgacacc acttcccacc cctggattcc catcccaaag taggtttacc tggaattgtg	6003
gtaggaatac taaaaagggg gaagtgagat agtgacacta tgacttaaca catgtcaaat	6063
gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaattc	6123
tgactctaac cctgtgactc tggggcagtc atttctcttg ggcttttctt tatcttaaaa	6183
aatgagagtt tccagctctt gtctgattct aagcctggat ccagtagctc tgactctacc	6243
tggaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgccctc	6303
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc	6352
Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala	
440 445	
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat	6400
Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr	
450 455 460	
cgc tat ggc tcc ttt tcc ctg acc ctg gac att gtc c gtgagtcttg	6447
Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val	
465 470 475	
cctacattgt ccgtaagctg gtggagggag gcgtgtgctg cttaggggtg cccagtggaa	6507
gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggtttc	6567
atatgaaggc agaatgggat tagggaggca gcccgaggac cttcctggcc atgggccttg	6627
ggggagggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag	6682
Gln	
ggg att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga	6730
Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly	
480 485 490	
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc	6775
Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly	
495 500	
5056-1000	
cacggttgcc ctgagaactc ctggggtgac tgetgtcctg ttctctggtg tctagtgtcc	6835
cttcccagat tccctgacgt aagctgacat ctctcccag g cta ccc aag gaa gcc	6890
Leu Pro Lys Glu Ala	
510	
tgc atg gac atc tca tgc cca ggg tgt cag ctg cct gcc cag cgg ctg	6938
Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu	
515 520 525	
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag	6986
Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln	
530 535 540	
gta ctg aag ggt ggc tca ggg acc tac tgc ctg aat gtg tct ttg gct	7034
Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala	
545 550 555	

from sequence 3

10/565,646 3

440	445	
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat		6400
Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr		
450	455	460
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg		6447
Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val		
465	470	475
cctacattgt ccgtaagctg gtggagggag gcgtgtgctg cttagggttg cccagtggaa		6507
gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggtttc		6567
atatgaaggc agaatgggat tagggaggca gcccgaggac cttcctggcc atgggccttg		6627
ggggaggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag		6682
	Gln	
ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga		6730
Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly		
480	485	490
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc		6775
Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly		
495	500	
	SOS ← insert	
cacggttgcc ctgagaactc ctggggtgac tgctgtcctg ttctctggtg tctagtgtcc		6835
cttcccagat tccctgacgt aagctgacat ctctcccag g cta ccc aag gaa gcc		6890
	Leu Pro Lys Glu Ala	
	510	
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg		6938
Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu		
515	520	525
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag		6986
Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln		
530	535	540
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct		7034
Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala		
545	550	555
gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g		7080
Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro		
560	565	570
gtaggtagtt ggacaagagg taggatgaag acacggggag atggtagagg ttacctacta		7140
gaggaagcag aactgaatg cagccgtatc tgggattcca cccatag gg caa gaa		7195
	Gly Gln Glu	
	575	
gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta		7243

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5

ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag ctc aga att 2369
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Ile
25 ← insert 30 35 40

cct gac tgc tgg aga g gtaggaactt ggcaatttcc agggaggata tgggtggaaat 2473
Pro Asp Cys Trp Arg
60

gggtggggag gqgaacgggg ttqaatgtac ttaqgaagat agqgaaggaa aaggcataca 2533

10/365, 646
from seq 5 8

cccagtcctcc ttgaccagt aaccccccttc cctactcttc ttcccaaaaa cctcag ac	4313
Asp	
caa tac tgg caa gtt ctg ggg ggc cca gtg tct gga ctg agc atc ggg	4361
Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly	
160 165 170	
aca gac aag gca atg ctg ggc aca tat aac atg gaa gtg act gtc tac	4409
Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr	
175 180 185	
cac cgc cgg ggg tcc cag agc tat gtg ccc ctc gct cac tcc agt tca	4457
His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser	
190 195 200	
gcc ttc acc att act g gtaaggactg aggaggggac aaggccagtt gcagggcagg	4513
Ala Phe Thr Ile Thr	
205	
agaaggtggg gaggtctgggc tggacaggaa aggggaaaga ggaaatggtg tgtaacctta	4573
caggggcaga accaggaaga tgtgggcaga gggatgtggg gcttgagacc cgtgaagggc	4633
caggcagctt gggttggttg aaaaatatgg ctgtgaaaga agaagctgac agaaagaaga	4693
acttatgggtt ctcactttct ctgactccaa tccag ac cag gtg ccc ttc tct	4746
Asp Gln Val Pro Phe Ser	
210 ← insert 215	
gtg agt gtg tct cag ctg cag gcc ttg gat gga agg aac aag cgc ttc	4794
Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly Arg Asn Lys Arg Phe	
220 225 230	
ctg aga aag cag cct ctg acc ttt gcc ctc cag ctc cat gat ccc agt	4842
Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser	
235 240 245	
ggc tat ttg gct ggg gct gac ctt tcc tac acc tgg gac ttt ggt gac	4890
Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp	
250 255 260	
agt aca ggg acc ctg atc tct cgg gca ctc acg gtc act cac act tac	4938
Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr Val Thr His Thr Tyr	
265 270 275	
cta gag tct ggc cca gtc act gca cag gtg gtg ctg cag gct gcc att	4986
Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile	
280 285 290 295	
cct ctc acc tcc tgt ggc tcc tct cca gtt cca ggc act aca gat agg	5034
Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Arg	
300 305 310	
cat gtg aca act gca gag gct cct gga acc aca gct ggc caa gtg cct	5082
His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr Ala Gly Gln Val Pro	
315 320 325	
act aca gaa gtc atg ggc acc aca cct ggc cag gtg cca act gca gag	5130

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/565,646

DATE: 01/30/2006

TIME: 16:00:02

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\01302006\J565646.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:23
 L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
 L:40 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
 L:45 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:38
 L:50 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:43
 L:55 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:48
 L:60 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:53
 L:65 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:58
 L:70 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:63
 L:75 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:68
 L:75 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:73
 L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:535 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:528
 L:540 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:533
 L:545 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:538
 L:550 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:543
 L:555 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:548
 L:560 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:553
 L:565 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:558
 L:570 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:563
 L:575 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:568
 L:580 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:573
 L:580 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:578
 L:699 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3
 L:823 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:1036 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1028
 L:1041 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1034
 L:1046 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1039
 L:1051 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1044
 L:1056 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1049
 L:1061 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1054
 L:1066 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1059
 L:1071 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1064
 L:1076 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1069
 L:1081 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1074
 L:1081 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1079
 L:1130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:1224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:1373 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 5
 L:1605 M:254 E: No. of Bases conflict, this line has no nucleotides.